IN THE CLAIMS

Please amend the claims as follows. The following listing of claims replaces all prior versions.

1-19. (Canceled).

20. (Withdrawn) A method for assessing the amount of a nucleic acid analyte in a sample comprising:

contacting a set of primers and a sample containing the nucleic acid analyte to amplify the analyte; and

detecting the amplified analyte or its complement by means of a probe, characterized in that the probe comprises:

one or more nucleotides and/or nucleotide analogues, selected from 2' -O-methyl nucleotides or LNA nucleotides, that have an affinity increasing modification; and

one or more unmodified nucleotides

thereby assessing the amount of nucleic acid analyte in the sample.

21. (Withdrawn) A method for assessing the presence of a nucleic acid analyte in a sample comprising:

contacting a set of primers and a sample containing the nucleic acid analyte to amplify the analyte; and

detecting the amplified analyte or its complement by means of a probe, characterized in that the probe comprises:

one or more nucleotides and/or nucleotide analogues, selected from 2' -O-methyl nucleotides or LNA nucleotides, that have an affinity increasing modification, wherein at a constant temperature of hybridization, the melting temperature of the probe with any possible analyte's polymorphism is increased compared to the melting temperature of an unmodified probe with any analyte's polymorphism; and

one or more unmodified nucleotides;

thereby assessing the presence of nucleic acid analyte in the sample.

22. (Withdrawn) The method of claim 20, wherein the probe is a molecular beacon.

23. (Withdrawn) The method of claim 21, wherein the probe is a molecular beacon.

24. (Withdrawn) A method for assessing the presence of a nucleic acid analyte in a sample using a molecular beacon probe that lowers the possible opening of the stem of the molecular beacon that results from at least one contaminant present in the amplification enzyme mixture, the method comprising

contacting a set of primers and a sample containing the nucleic acid analyte to amplify the analyte; and

detecting the amplified analyte or its complement by means of the probe, characterized in that the probe's stem comprises:

one or more nucleotides and/or nucleotide analogues that have an affinity increasing modification, especially 2' -O-methyl nucleotides; and

one or more unmodified nucleotides;

thereby assessing the presence of nucleic acid analyte in the sample.

25. (Withdrawn) A method for assessing the presence of a nucleic acid analyte in a sample using a molecular beacon probe for lowering:

the effect of sequence variations in a nucleic acid analyte, and/or

the possible opening of the stem-loop structure of the molecular beacon that results from at least one contaminant present in the amplification enzymes mixture, the method comprising

contacting a set of primers and a sample containing the nucleic acid analyte to amplify the analyte; and

detecting the amplified analyte or its complement by means of the probe, characterized in that the probe's loop comprises:

one or more nucleotides and/or nucleotide analogues that have an affinity increasing modification, and

one or more unmodified nucleotides

and/or the probe's stem comprises:

one or more nucleotides and/or nucleotide analogues that have an affinity increasing modification, especially 2' –O-methyl nucleotides, and

one or more unmodified nucleotides;

thereby assessing the presence of nucleic acid analyte in the sample.

26. (Withdrawn) The method of claim 20 wherein the diagnostic assay is a homogenous assay.

27. (Withdrawn) The method of claim 21 wherein the diagnostic assay is a homogenous assay.

28. (Withdrawn) The method of claim 24 wherein the diagnostic assay is a homogenous assay.

29. (Withdrawn) The method of claim 25 wherein the diagnostic assay is a homogenous assay.

30. (Withdrawn) The method of claim 20 wherein the diagnostic assay is a heterogeneous assay.

31. (Withdrawn) The method of claim 21 wherein the diagnostic assay is a heterogeneous assay.

32. (Withdrawn) The method of claim 24 wherein the diagnostic assay is a heterogeneous assay.

33. (Withdrawn) The method of claim 25 wherein the diagnostic assay is a heterogeneous assay.

34. (Withdrawn) The method of claim 20, wherein the nucleotides or nucleotide analogues having an affinity increasing modification are selected from the group consisting of 2' –O-derivatized nucleotides, locked nucleic acids and peptide nucleic acids.

35. (Withdrawn) The method of claim 21, wherein the nucleotides or nucleotide analogues having an affinity increasing modification are selected from the group consisting of 2' –O-derivatized nucleotides, locked nucleic acids and peptide nucleic acids.

36. (Withdrawn) The method of claim 24, wherein the nucleotides or nucleotide analogues having an affinity increasing modification are selected from the group consisting of 2' –O-derivatized nucleotides, locked nucleic acids and peptide nucleic acids.

37. (Withdrawn) The method of claim 25, wherein the nucleotides or nucleotide analogues having an affinity increasing modification are selected from the group consisting of 2' –O-derivatized nucleotides, locked nucleic acids and peptide nucleic acids.

38. (Withdrawn) The method of claim 34, wherein the 2' –O-derivatized nucleotide is a 2' –O-methyl-nucleotide.

39. (Canceled).

40. (Currently amended) A molecular beacon probe, comprising:

a stem comprising ~~said probe allowing the lowering of the possible opening of the stem-loop structure of the molecular beacon that results from at least one contaminant present in the amplification enzyme mixture,~~

~~characterized in that the probe's stem comprises:~~

one or more nucleotides or nucleotide analogues having an affinity increasing modification, wherein said one or more nucleotides or nucleotide analogues are selected from the group consisting of a 2' –O-derivatized nucleotide, a locked nucleic acid, and a peptide nucleic acid, and

one or more unmodified nucleotides,

wherein each base pair of said stem comprises no more than one 2' –O-methyl nucleotide,

further wherein said probe has better stability and does not open spontaneously in the presence of contaminants present in an amplification enzyme mixture comprising said molecular beacon probe as compared to a molecular beacon probe without said stem.

41. (Currently amended) A molecular beacon probe comprising a stem and a loop, wherein said ~~probe allowing the lowering of:~~

~~the effect of sequence variations in a nucleic acid analyte, and/or~~

~~the possible opening of the stem-loop structure of the molecular beacon characterized in that the probe's~~ loop comprises:

one or more nucleotides and/or nucleotide analogues that have an affinity increasing modification, and one or more unmodified nucleotides; and

~~one or more unmodified nucleotides~~

~~and/or the probe's~~ said stem comprises:

one or more 2'-O-methyl nucleotides, and

one or more unmodified nucleotides,

wherein each base pair of said stem comprises no more than one 2'-O-methyl nucleotide,

wherein the sensitivity of said probe to polymorphisms in the target nucleic acid sequence is lowered as compared to a molecular beacon probe without said loop and wherein the spontaneous opening of the probe in the presence of contaminants present in an amplification enzyme mixture comprising said molecular beacon probe is lowered as compared to a molecular beacon probe without said stem.

42. (Canceled).

43. (Previously Presented) The molecular beacon probe as claimed in claim 41, wherein the nucleotides or nucleotide analogues having an affinity increasing modification are selected from the group consisting of 2' –O-derivatized nucleotides, locked nucleic acids, and peptide nucleic acids.

44. (Currently amended) The molecular beacon probe as claimed in claim [[42]]40, wherein the 2' –O-derivatized nucleotide is a 2' –O-methyl-nucleotide.

45-46. (Canceled).

47. (Previously Presented) The molecular beacon probe as claimed in claim 40, wherein at least one base pair constituting the stem contains no nucleotide or nucleotide analogue having an affinity increasing modification.

48. (Previously Presented) The molecular beacon probe as claimed in claim 41, wherein at least one base pair constituting the stem contains no nucleotide or nucleotide analogue having an affinity increasing modification.

49. (Previously Presented) The molecular beacon probe as claimed in claim 40, wherein one base pair constituting the stem contains no nucleotide or nucleotide analogue having an affinity increasing modification.

50. (Previously Presented) The molecular beacon probe as claimed in claim 41, wherein one base pair constituting the stem contains no nucleotide or nucleotide analogue having an affinity increasing modification.

51. (Previously Presented) The molecular beacon probe as claimed in claim 40, wherein each strand constituting the stem contains at least one nucleotide or nucleotide analogue having an affinity increasing modification.

52. (Previously Presented) The molecular beacon probe as claimed in claim 41, wherein each strand constituting the stem contains at least one nucleotide or nucleotide analogue having an affinity increasing modification.

53. (Canceled).

54. (Previously Presented) A kit for performing a diagnostic amplification assay, comprising the appropriate primers, polymerase(s) and reagents for performing amplification of an analyte to be diagnosed and a probe or a molecular probe as claimed in claim 40 for detecting the amplified analyte.

55. (Previously Presented) A kit for performing a diagnostic amplification assay, comprising the appropriate primers, polymerase(s) and reagents for performing amplification of an analyte to be diagnosed and a probe or a molecular probe as claimed in claim 41 for detecting the amplified analyte.

56. (New) A molecular beacon probe comprising a stem and a loop, wherein said loop comprises:

one or more nucleotides and/or nucleotide analogues that have an affinity increasing modification, and one or more unmodified nucleotides; or

said stem comprises:

one or more 2'-O-methyl nucleotides, and

one or more unmodified nucleotides,

wherein each base pair of said stem comprises no more than one 2'-O-methyl nucleotide;

wherein the sensitivity of said probe to polymorphisms in the target nucleic acid sequence is lowered as compared to a molecular beacon probe without said loop or wherein the spontaneous opening of the probe in the presence of contaminants present in an amplification enzyme mixture comprising said molecular beacon probe is lowered as compared to a molecular beacon probe without said stem.